

SEQUENCE LISTING

<110> Sprecher, Cindy A.
 Presnell, Scott R.
 Gao, Zeren
 Whitmore, Theodore E.
 Kuijper, Joseph L.
 Maurer, Mark F.

<120> CYTOKINE RECEPTOR ZCYTOR17

<130> 00-42

<150> US 60/214,282

<151> 2000-06-26

<150> US 60/214,955

<151> 2000-06-29

<150> US 60/267,963

<151> 2001-08-02

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aatgtccgca aaacattctc tctccccagc ctctcatgtgt taacctgggg atg atg      176
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tgg acc tgg gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg      224
Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu
      5              10              15
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gca gct ctg cca gct aag cct gag aac att tcc tgt gtc tac tac tat      272
Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr
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agg aaa aat tta acc tgc act tgg agt cca gga aag gaa acc agt tat      320
Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Ala Gly Lys Glu Thr Ser Tyr
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acc cag tac aca gtt aag aga act tac gct ttt gga gaa aaa cat gat      368
Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp
      55              60              65
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Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser
      70              75              80
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gaa gct gaa aat gga gat ggt gta att aaa tct cat atg aca tac tgg Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp 100 105 110	512
aga tta gag aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val 115 120 125 130	560
aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa tgg ata aag Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys 135 140 145	608
cct gag ttg gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe 150 155 160	656
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cgt aag gat aaa aac caa acg tac aac ctc acg ggg ctg cag cct ttt Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe 180 185 190	752
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gga aga agg cca gtg cgg ttg tta tgg aag aag gca aga gga gcc cca Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro 245 250 255	944
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Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr			
340 345 350			
tgg atg att gaa tgg ttt ccg gat gtg gac tca gag ccc acc acc ctt			1280
Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu			
355 360 365 370			
tcc tgg gaa tct gtg tct cag gcc acg aac tgg acg atc cag caa gat			1328
Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp			
375 380 385			
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Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu			
390 395 400			
cat gac aaa gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa			1424
His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu			
405 410 415			
ggc gtt cca tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg			1472
Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val			
420 425 430			
aag acg gtc acg atc aca tgg aaa gag att ccc aag agt gag aga aag			1520
Lys Thr Val Thr Ile Thr Lys Glu Ile Pro Lys Ser Glu Arg Lys			
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ggg atc atc tgc aac tac acc atc ttt tac caa gct gaa ggt gga aaa			1568
Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys			
455 460 465			
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Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu			
470 475 480			
tcc ctg aaa cga aag acc tct tac att gtt cag gtc atg gcc agc acc			1664
Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr			
485 490 495			
agt gct ggg gga acc aac ggg acc agc ata aat ttc aag aca ttg tca			1712
Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser			
500 505 510			
ttc agt gtc ttt gag att atc ctc ata act tct ctg att ggt gga ggc			1760
Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly			
515 520 525 530			
ctt ctt att ctc att atc ctg aca gtg gca tat ggt ctc aaa aaa ccc			1808
Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro			
535 540 545			
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Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu			
550 555 560			
agt agt ata gcc aca tgg cat gga gat gat ttc aag gat aag cta aac			1904
Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn			
565 570 575			

ctg aag gag tct gat gac tct gtg aac aca gaa gac agg atc tta aaa	1952
Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys	
580 585 590	
cca tgt tcc acc ccc agt gac aag ttg gtg att gac aag ttg gtg gtg	2000
Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val	
595 600 605 610	
aac ttt ggg aat gtt ctg caa gaa att ttc aca gat gaa gcc aga acg	2048
Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr	
615 620 625	
ggg cag gaa aac aat tta gga ggg gaa aag aat ggg tat gtg acc tgc	2096
Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Tyr Val Thr Cys	
630 635 640	
ccc ttc agg cct gat tgt ccc ctg ggg aaa agt ttt gag gag ctc cca	2144
Pro Phe Arg Pro Asp Cys Pro Leu Gly Lys Ser Phe Glu Glu Leu Pro	
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gtt tca cct gag att ccg ccc aga aaa tcc caa tac cta cgt tcg agg	2192
Val Ser Pro Glu Ile Pro Pro Arg Lys Ser Gln Tyr Leu Arg Ser Arg	
660 665 670	
atg cca gag ggg acc cgc cca gaa gcc aaa gag cag ctt ctc ttt tct	2240
Met Pro Glu Gly Thr Arg Pro Glu Ala Lys Glu Gln Leu Leu Phe Ser	
675 680 685 690	
ggg caa agt tta gta cca gat cat ctg tgt gag gaa gga gcc cca aat	2288
Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala Pro Asn	
695 700 705	
cca tat ttg aaa aat tca gtg aca gcc agg gaa ttt ctt gtg tct gaa	2336
Pro Tyr Leu Lys Asn Ser Val Thr Ala Arg Glu Phe Leu Val Ser Glu	
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aaa ctt cca gag cac acc aag gga gaa gtc taaatgcgac catagcátga	2386
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Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr	
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Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys	
50 55 60	
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser	
65 70 75 80	
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile	
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Arg	Val	Lys	Pro	Val	Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp
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Arg	Phe	Arg	Thr	Val	Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala
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Lys	Asn	Arg	Lys	Asp	Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln
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Pro	Phe	Thr	Glu	Tyr	Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser
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Lys	Phe	Trp	Ser	Asp	Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu
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Glu	Ala	Pro	Cys	Gly	Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu
225					230					235					240
Ala	Asp	Gly	Arg	Arg	Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly
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Ala	Pro	Val	Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro
			260					265						270	
Glu	Ser	Asn	Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln
			275				280								
Leu	Glu	Leu	His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser
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Tyr	Asn	Ser	Leu	Gly	Lys	Ser	Pro	Val	Ala	Thr	Leu	Arg	Ile	Pro	Ala
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Ile	Gln	Glu	Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val
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Ala	Glu	Asp	Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val
			340					345					350		
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Thr	Leu	Ser	Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln
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Gln	Asp	Lys	Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	Pro
385					390					395					400
Met	Leu	His	Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala
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Lys	Glu	Gly	Val	Pro	Ser	Glu	Gly	Pro	Glu	Thr	Lys	Val	Glu	Asn	Ile
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Arg	Lys	Gly	Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly
						455					460				
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Leu	Glu	Ser	Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala
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Lys	Pro	Asn	Lys	Leu	Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	Pro
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Ala	Glu	Ser	Ser	Ile	Ala	Thr	Trp	His	Gly	Asp	Asp	Phe	Lys	Asp	Lys
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Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala
    610                                615                620
Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Tyr Val
    625                                630                635                640
Thr Cys Pro Phe Arg Pro Asp Cys Pro Leu Gly Lys Ser Phe Glu Glu
    645                                650                655
Leu Pro Val Ser Pro Glu Ile Pro Pro Arg Lys Ser Gln Tyr Leu Arg
    660                                665                670
Ser Arg Met Pro Glu Gly Thr Arg Pro Glu Ala Lys Glu Gln Leu Leu
    675                                680                685
Phe Ser Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala
    690                                695                700
Pro Asn Pro Tyr Leu Lys Asn Ser Val Thr Ala Arg Glu Phe Leu Val
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<210> 3
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<221> VARIANT
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<210> 4
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<221> misc_feature
<222> (1)...(2196)
<223> n = A,T,C or G

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acntggwsnc cnggnaarga racnwsntay acncartaya cngtnaarmg nacntaygcn      180
ttyggngara arcaygayaa ytgyacnacn aaywsnwsna cnwsngaraa ymgngcnwsn      240
tgywsnttyt tyytnccnmg nathacnath ccngayaayt ayacnathga rgtngargcn      300
garaayggng ayggngtnat haarwsncay atgacntayt ggmngnytna raayathgcn      360
aaracngarc cncncaarat htymngngtn aarccngtny tnggnathaa rmgnatgath      420
carathgart ggathaarcc ngarytngcn ccngtnwsnw sngayytnaa rtayacnytn      480
mgnttymgna cngtnaayws nacnwsntgg atggargtna ayttygcnaa raaymgnaar      540
gayaaraayc aracntayaa yytnacnggn ytnrcarcent tyacngarta ygtnathgcn      600
ytnmgntgyg cngtnaarga rwsnaartty tggwsngayt ggwsncarga raaratgggn      660
atgacngarg argargcncc ntgyggnytn garytntggm gngtnytnaa rccngcngar      720
gcngayggnm gnmngccngt nmgnytnytn tggaaraarg cnmgngggngc nccngtnytn      780
garaaracny tnggntayaa yathtggtay tayccngarw snaayacnaa yytnacngar      840

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acnatgaaya	cnacnaayca	rcarytngar	ytncayytng	gnggngarws	nttytgggtn	900
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athcargara	arwsnttyca	rtgyathgar	gtnatgcarg	cntgygtngc	ngargaycar	1020
ytngtngtna	artggcarws	nwsngcnytn	gaygtnaaya	cntggatgat	hgartggtty	1080
ccngaygtng	aywsngarcc	nacnacnytn	wsntgggarw	sngtnwsnca	rgcnacnaay	1140
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gayaarytng	tnathgayaa	rytngtngtn	aayttyggna	aygtynytnca	rgarathtty	1860
acngaygarg	cnmggnacngg	ncargaraay	aayytnggng	gngaraaraa	yggntaygtn	1920
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ccngarathc	cncnmgnaa	rwsncartay	ytnmgwnsnm	gnatgccnga	rggnacnmgn	2040
ccngargcna	argarcaryt	nytnttywsn	ggncarwsny	tngtnccnga	ycayytntgy	2100
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<212> DNA

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<223> Oligonucleotide primer ZC12701

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20

<210> 6

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC27898

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<210> 7

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<212> DNA

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<223> Oligonucleotide primer ZC14063

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<210> 8

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC27899

<400> 8

ccagaacttt gactccttga ccg

23

<210> 9

<211> 765

<212> DNA

<213> Homo sapiens

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gaataacgat	cccagataat	tataccattg	aggtggaagc	tgaaaatgga	gatgggtgta	480
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<213> Artificial Sequence

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<223> Oligonucleotide primer ZC6346

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<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28480

<400> 12

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24

<210> 13

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<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC26405

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<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC27895

<400> 14

gaagtcaact tcgctaagaa ccg

23

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC5020

<400> 15

cactggagtg gcaacttcca g

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<210> 16

<211> 1853

<212> DNA

<213> Homo sapiens

<400> 16

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tgactggagc	caagaaaaaa	tgggaatgac	tgagggaagaa	gctccatgtg	gcctggaact	180
gtggggagtc	ctgaaaccag	ctgaggcgga	tgggaagaagg	ccagtgcggt	tggtatggaa	240
gaaggcaaga	ggagccccag	tcctagagaa	aacacttgge	tacaacatat	ggtactatcc	300
agaaagcaac	actaacctca	cagaaacaat	gaacactact	aaccagcagc	ttgaactgca	360
tctgggaggc	gagagctttt	gggtgtctat	gatttcttat	aattctcttg	ggaagtctcc	420
agtggccacc	ctgaggattc	cagctattca	agaaaaatca	tttcagtgca	ttgagggtcat	480
gcaggcctgc	gttgctgagg	accagctagt	ggtgaagtgg	caaagctctg	ctctagacgt	540
gaacacttgg	atgattgaat	ggtttccgga	tgtggactca	gagcccacca	ccctttcctg	600
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ccaggcttat	gccaagaag	gcgttccatc	agaaggctct	gagaccaagg	tggagaacat	780
tggcgtgaag	acggtcacga	tcacatggag	agagattccc	aagagtgaga	gaaaggggat	840
catctgcaac	tacaccatct	tttaccaagc	tgaagggtga	aaaggattct	ccaagacagt	900
caattccagc	atcttgcagt	acggcctgga	gtccctgaaa	cgaaagacct	cttacattgt	960
tcaggctcatg	gccagcacca	gtgctggggg	aaccaacggg	accagcataa	atttcaagac	1020
attgtcattc	agtgtctttg	agattatcct	cataacttct	ctgattgggtg	gaggccttct	1080
tattctcatt	atcctgacag	tggcatatgg	tctcaaaaaa	cccaacaaat	tgactcatct	1140
gtgttggccc	accgttccca	accctgctga	gagtagtata	gccacacggc	atggagatga	1200
tttcaaggat	aagctaaacc	tgaaggagtc	tgatgactct	gtgaacacag	aagacaggat	1260
cttaaaacca	tgttccaccc	ccagtgcaca	tgttggtgatt	gacaagttgg	tggtgaactt	1320
tgggaatggt	tgtcaagaaa	ttttcacaga	tgaagccaga	acgggtcagg	aaaacaattt	1380
aggaggggaa	aagaatggga	ctagaattct	gtcttctctg	ccaacttcaa	tataagtgtg	1440
gactaaaatg	cgagaaagg	gtcctgtggg	ctatgcaaat	tagaaaggac	atgcagagtt	1500
ttccaactag	gaagactgaa	tctgtggccc	caagagaacc	atctctgaag	actgggtatg	1560

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tgggtcttttc cacacatgga ccacctacgg atgtaatctg taatgcatgt gcatgagaag 1620
tctgttatta agtagagtgt gaaaacatgg ttatggtaat aggaacagct tttaaaatgc 1680
ttttgcatgt gggcctttca tacaaaaaag ccataatacc attttcatgt aatgctatac 1740
ttctatacta ttttcatgta atactatact tctatactat tttcatgtaa tactatactt 1800
ctatactatt ttcatgtaat actatacttc tatattaaag ttttaccac tca 1853

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<210> 17
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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (162)...(1133)

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aaaacattct ctctccccag ctttcatgtg ttaacctggg g atg atg tgg acc tgg 176
Met Met Trp Thr Trp
1 5

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gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224
Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu
10 15 20

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cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272
Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn
25 30 35

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```

tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320
Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr
40 45 50

```

```

aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368
Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr
55 60 65

```

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acc aat agt tct ada agt gaa aat cgt gct tgc tgc tct ttt ttc ctt 416
Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu
70 75 80 85

```

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cca aga ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa 464
Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu
90 95 100

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```

aat gga gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag 512
Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu
105 110 115

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aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt 560
Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val
120 125 130

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ttg ggc atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg 608
Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu
135 140 145

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gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc 656
Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val
150 155 160 165

```

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aac agt acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat      704
Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp
170                               175                               180

aaa aac caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat      752
Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr
185                               190                               195

gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac      800
Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp
200                               205                               210

tgg agc caa gaa aaa atg gga atg act gag gaa gaa gct cca tgt ggc      848
Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro Cys Gly
215                               220                               225

ctg gaa ctg tgg aga gtc ctg aaa cca gct gag gcg gat gga aga agg      896
Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly Arg Arg
230                               235                               240                               245

cca gtg cgg ttg tta tgg aag aag gca aga gga gcc cca gtc cta gag      944
Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu Glu
250                               255                               260

aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac act aac      992
Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn Thr Asn
265                               270                               275

ctc aca gaa aca atg aac act act aac cag cag ctt gaa ctg cat ctg      1040
Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu His Leu
280                               285                               290

gga ggc gag agc ttt tgg gtg tct atg att tct tat aat tct ctt ggg      1088
Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser Leu Gly
295                               300                               305

aag tct cca gtg gcc acc ctg agg att cca gct att caa gaa aaa      1133
Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu Lys
310                               315                               320

tagaaacttt acagatgcta gtcccagaca taaaagaaaa taatgttctg gatgtgcacg      1193
atggctcacg cctgtaatcc cagcactttg aggccaagac gggtggatcg ctgagttcag      1253
gagttcaaga caagtccagg caacatagtg aaaccttggt tctaca                      1299

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<210> 18
<211> 324
<212> PRT
<213> Homo sapiens

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<400> 18
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1      5      10      15
Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr
20     25     30
Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr
35     40     45
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
50     55     60
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
65     70     75     80
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
85     90     95

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Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
 100 105 110
 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
 115 120 125
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
 130 135 140
 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
 145 150 155 160
 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
 165 170 175
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
 180 185 190
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
 195 200 205
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
 210 215 220
 Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu
 225 230 235 240
 Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly
 245 250 255
 Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro
 260 265 270
 Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln
 275 280 285
 Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser
 290 295 300
 Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala
 305 310 315 320
 Ile Gln Glu Lys

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC27897

<400> 19

caagctactt ctctggtgta tgg

23

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28521

<400> 20

gagtagtagc tccaggattc ac

22

<210> 21

<211> 1476

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (162)...(878)

<400> 21

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aaaacattct ctctccccag ccttcatgtg ttaacctggg g atg atg tgg acc tgg	176
Met Met Trp Thr Trp	
1 5	
gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg	224
Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu	
10 15 20	
cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat	272
Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn	
25 30 35	
tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac	320
Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr	
40 45 50	
aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca	368
Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr	
55 60 65	
acc aat agt tct aca agt gaa aat cgt gct tgc tgc tct ttt ttc ctt	416
Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu	
70 75 80 85	
cca aga ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa	464
Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu	
90 95 100	
aat gga gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag	512
Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu	
105 110 115	
aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt	560
Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val	
120 125 130	
ttg ggc atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg	608
Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu	
135 140 145	
gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc	656
Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val	
150 155 160 165	
aac agt acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat	704
Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp	
170 175 180	
aaa aac caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat	752
Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr	
185 190 195	
gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac	800
Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp	
200 205 210	
tgg agc caa gaa aaa atg gga atg act gag gaa gaa ggc aag cta ctc	848
Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Gly Lys Leu Leu	
215 220 225	

cct gcg att ccc gtc ctg tct gct ctg gtg tagggctgct ttgggctaga 898
 Pro Ala Ile Pro Val Leu Ser Ala Leu Val
 230 235

cttgggtgggg tttgtcacca cctgggttggg aatcatggaa tctcatgacc ccagggggccc 958
 cctgtaccat cgagagtggag cctgcacaac tttgtgcccc aaaggcaaag gatcacattt 1018
 taatactcat gaggttctta tactatacat gaaagggtat catatcattt gttttgtttt 1078
 gttttgtttt tgagatggag tcttactctg tcaccaggga tggagtgcag tgatgtgatc 1138
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 aagggatata accatgttgg ctaggctagt cttgaactcc tgacctcagg taatctgccc 1318
 accttgacct cccaaagtgt tgggattaca ggcgtgagcc actgtgcccc gccagtatca 1378
 tatcatctga aggtatcctg tgataaatta aagatacata ttgtgaatcc tggagctact 1438
 actcaaaaaa taaataaagg tgtaactaat acaattta 1476

<210> 22
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 22
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 Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr
 20 25 30
 Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr
 35 40 45
 Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
 50 55 60
 His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
 65 70 75 80
 Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
 85 90 95
 Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
 100 105 110
 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
 115 120 125
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
 130 135 140
 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
 145 150 155 160
 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
 165 170 175
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
 180 185 190
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
 195 200 205
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
 210 215 220
 Glu Gly Lys Leu Leu Pro Ala Ile Pro Val Leu Ser Ala Leu Val
 225 230 235

<210> 23
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC28575

<400> 23
 ccaggaaagg aaaccagtta tacc

<210> 24
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC27899

 <400> 24
 ccagaacttt gactccttga ccg 23

 <210> 25
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC14063

 <400> 25
 caccagacat aatagctgac agact 25

 <210> 26
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC17574

 <400> 26
 ggtrttgctc agcatgcaca c 21

 <210> 27
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC17600

 <400> 27
 catgtaggcc atgaggtcca ccac 24

 <210> 28
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC26358

 <400> 28
 aaaaccaaac gtacaacctc acggg 25

 <210> 29
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Oligonucleotide primer ZC26359
 <400> 29
 gagcagccat acaccagagc agaca 25
 <210> 30
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide primer ZC17212
 <400> 30
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 <210> 31
 <211> 30
 <212> DNA
 <213> Artificial Sequence
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 <223> Oligonucleotide primer ZC17313
 <400> 31
 caccctgcga agccttagca gcagtaggcc 30
 <210> 32
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide primer ZC17205
 <400> 32
 cccgcccat ccccgtaggac caccttggtg 30
 <210> 33
 <211> 30
 <212> DNA
 <213> Artificial Sequence
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 <223> Oligonucleotide primer ZC17206
 <400> 33
 gggctctagac cttcagggct gctgccaata 30
 <210> 34
 <211> 6
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Glu-Glu Tag peptide
 <400> 34
 Glu Tyr Met Pro Met Glu
 1 5
 <210> 35

<211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FLAG tag peptide sequence

<400> 35
 Asp Tyr Lys Asp Asp Asp Lys
 1 5

<210> 36
 <211> 699
 <212> DNA
 <213> Homo sapiens

<400> 36
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 ggggcaccgt cagtcttctt cttcccccca aaacccaagg acaccctcat gatctcccgg 120
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
 aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 240
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
 ggcaaggagt acaagtgcga ggtctccaac aaagccctcc catcctccat cgagaaaacc 360
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
 cccgtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc 600
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
 tacacgcaga agagcctctc cctgtctccg ggtaaataa 699

<210> 37
 <211> 990
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(990)

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 1 5 10 15
 agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac 96
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc 144
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc 192
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc 240
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag 288
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys

85								90					95					
aaa	ggt	gag	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	336		
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys			
			100				105						110					
cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	384		
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro			
			115				120						125					
aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	432		
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys			
			130				135						140					
gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	480		
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp			
			145				150						155			160		
tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	528		
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu			
			165				170						175					
gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	576		
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu			
			180				185						190					
cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	624		
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn			
			195				200						205					
aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	672		
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly			
			210				215						220					
cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	720		
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu			
			225				230						235			240		
ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	768		
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr			
			245				250						255					
ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	816		
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn			
			260				265						270					
aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	864		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe			
			275				280						285					
ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	912		
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn			
			290				295						300					
gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	960		
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr			
			305				310						315			320		
cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa							990		
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 <211> 330
 <212> PRT
 <213> Homo sapiens

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 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
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 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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 <213> Homo sapiens

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Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	
			20					25					30			

ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg 144
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc 192
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa 240
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 65 70 75 80

cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc 288
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 85 90 95

gtc aca aag agc ttc aac agg gga gag tgt tag 321
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
100 105

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<210> 40
<211> 106
<212> PRT
<213> Homo sapiens
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Leu	Lys	Ser	Gly 20	Thr	Ala	Ser	Val	Val 25	Cys	Leu	Leu	Asn 30	Asn	Phe	Tyr	
Pro	Arg	Glu 35	Ala	Lys	Val	Gln	Trp 40	Lys	Val	Asp	Asn 45	Ala	Leu	Gln	Ser	
Gly	Asn 50	Ser	Gln	Glu	Ser 55	Val	Thr	Glu	Gln	Asp 60	Ser	Lys	Asp	Ser	Thr	
Tyr 65	Ser	Leu	Ser	Ser 70	Thr	Leu	Thr	Leu	Ser 75	Lys	Ala	Asp	Tyr	Glu	Lys 80	
His	Lys	Val	Tyr 85	Ala	Cys	Glu	Val	Thr 90	His	Gln	Gly	Leu	Ser 95	Ser	Pro	
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 <223> Oligonucleotide primer ZC12748
 <400> 44
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 cgcggtgtgta attccgggaa ggggagggat ttacgggaag 100
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 aaaacattct ctctccccag ccttcattgtg ttaacctggg g atg atg tgg acc tgg 176
 Met Met Trp Thr Trp
 1 5
 gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224
 Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu
 10 15 20
 cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272
 Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn
 25 30 35
 tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320
 Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr
 40 45 50
 aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368
 Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr
 55 60 65

acc	aat	agt	tct	aca	agt	gaa	aat	cgt	gct	tcg	tgc	tct	ttt	ttc	ctt	416
Thr	Asn	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser	Cys	Ser	Phe	Phe	Leu	
70					75					80					85	
cca	aga	ata	acg	atc	cca	gat	aat	tat	acc	att	gag	gtg	gaa	gct	gaa	464
Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu	Ala	Glu	
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aat	gga	gat	ggt	gta	att	aaa	tct	cat	atg	aca	tac	tgg	aga	tta	gag	512
Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg	Leu	Glu	
			105					110					115			
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Asn	Ile	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe	Arg	Val	Lys	Pro	Val	
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Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro	Glu	Leu	
	135					140					145					
gcg	cct	gtt	tca	tct	gat	tta	aaa	tac	aca	ctt	cga	ttc	agg	aca	gtc	656
Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg	Thr	Val	
150					155					160					165	
aac	agt	acc	agc	tgg	atg	gaa	gtc	aac	ttc	gct	aag	aac	cgt	aag	gat	704
Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg	Lys	Asp	
				170					175					180		
aaa	aac	caa	acg	tac	aac	ctc	acg	ggg	ctg	cag	cct	ttt	aca	gaa	tat	752
Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr	Glu	Tyr	
			185					190					195			
gtc	ata	gct	ctg	cga	tgt	gcg	gtc	aag	gag	tca	aag	ttc	tgg	agt	gac	800
Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp	Ser	Asp	
		200				205						210				
tgg	agc	caa	gaa	aaa	atg	gga	atg	act	gag	gaa	gaa	gct	cca	tgt	ggc	848
Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro	Cys	Gly	
	215					220					225					
ctg	gaa	ctg	tgg	aga	gtc	ctg	aaa	cca	gct	gag	gcg	gat	gga	aga	agg	896
Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly	Arg	Arg	
230					235					240					245	
cca	gtg	cgg	ttg	tta	tgg	aag	aag	gca	aga	gga	gcc	cca	gtc	cta	gag	944
Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	Leu	Glu	
				250					255					260		
aaa	aca	ctt	ggc	tac	aac	ata	tgg	tac	tat	cca	gaa	agc	aac	act	aac	992
Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	Glu	Ser	Asn	Thr	Asn	
			265					270					275			
ctc	aca	gaa	aca	atg	aac	act	act	aac	cag	cag	ctt	gaa	ctg	cat	ctg	1040
Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	Leu	Glu	Leu	His	Leu	
		280					285					290				
gga	ggc	gag	agc	ttt	tgg	gtg	tct	atg	att	tct	tat	aat	tct	ctt	ggg	1088
Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	Tyr	Asn	Ser	Leu	Gly	
	295					300					305					

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gtg gtg aag tgg caa agc tct gct cta gac gtg aac act tgg atg att Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp Met Ile 345 350 355	1232
gaa tgg ttt ccg gat gtg gac tca gag ccc acc acc ctt tcc tgg gaa Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser Trp Glu 360 365 370	1280
tct gtg tct cag gcc acg aac tgg acg atc cag caa gat aaa tta aaa Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys Leu Lys 375 380 385	1328
cct ttc tgg tgc tat aac atc tct gtg tat cca atg ttg cat gac aaa Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His Asp Lys 390 395 400 405	1376
gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa ggc gtt cca Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly Val Pro 410 415 420	1424
tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg aag acg gtc Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys Thr Val 425 430 435	1472
acg atc aca tgg aaa gag att ccc aag agt gag aga aag ggt atc atc Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly Ile Ile 440 445 450	1520
tgc aac tac acc atc ttt tac caa gct gaa ggt gga aaa gga ttc tcc Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly Phe Ser 455 460 465	1568
aag aca gtc aat tcc agc atc ttg cag tac ggc ctg gag tcc ctg aaa Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser Leu Lys 470 475 480 485	1616
cga aag acc tct tac att gtt cag gtc atg gcc agc acc agt gct ggg Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser Ala Gly 490 495 500	1664
gga acc aac ggg acc agc ata aat ttc aag aca ttg tca ttc agt gtc Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe Ser Val 505 510 515	1712
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ctc att atc ctg aca gtg gca tat ggt ctc aaa aaa ccc aac aaa ttg Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn Lys Leu 535 540 545	1808
act cat ctg tgt tgg ccc acc gtt ccc aac cct gct gaa agt agt ata Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser Ser Ile 1856	

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gcc aca tgg cat gga gat gat ttc aag gat aag cta aac ctg aag gag				1904
Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu Lys Glu	570	575	580	
tct gat gac tct gtg aac aca gaa gac agg atc tta aaa cca tgt tcc				1952
Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro Cys Ser	585	590	595	
acc ccc agt gac aag ttg gtg att gac aag ttg gtg gtg aac ttt ggg				2000
Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn Phe Gly	600	605	610	
aat gtt ctg caa gaa att ttc aca gat gaa gcc aga acg ggt cag gaa				2048
Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly Gln Glu	615	620	625	
aac aat tta gga ggg gaa aag aat ggg act aga att ctg tct tcc tgc				2096
Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser Ser Cys	630	635	640	645
cca act tca ata taagtgtgga ctaaaatgcg agaaaggtgt cctgtggtct				2148
Pro Thr Ser Ile				

atgcaaatta gaaaggacat gcagagtttt ccaactagga agactgaatc tgtggcccca	2208
agagaacccat ctctgaagac tgggtatgtg gtctttttcca cacatggacc acctacggat	2268
gcaatctgta atgcatgtgc atgagaagtc tggtattaag tagagtgtga aaacatgggt	2328
atggtaatag gaacagcttt taaaatgctt ttgtatttgg gcctttcata caaaaaagcc	2388
ataataccat tttcatgtaa tgctatactt ctatactatt ttcattgtaat actatacttc	2448
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 <212> PRT
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35 Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys	50
50 His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser	65
65 Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile	80
80 Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr	100
100 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe	115
115 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp	130
130 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu	145
145 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala	160
165	175

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Glu	Ala	Pro	Cys	Gly	Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu
225					230					235					240
Ala	Asp	Gly	Arg	Arg	Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly
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Ala	Pro	Val	Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro
			260					265					270		
Glu	Ser	Asn	Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln
		275					280					285			
Leu	Glu	Leu	His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser
	290					295					300				
Tyr	Asn	Ser	Leu	Gly	Lys	Ser	Pro	Val	Ala	Thr	Leu	Arg	Ile	Pro	Ala
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Ile	Gln	Glu	Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val
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Ala	Glu	Asp	Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val
			340					345						350	
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Thr	Leu	Ser	Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln
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Gln	Asp	Lys	Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	Pro
385					390					395					400
Met	Leu	His	Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala
				405					410					415	
Lys	Glu	Gly	Val	Pro	Ser	Glu	Gly	Pro	Glu	Thr	Lys	Val	Glu	Asn	Ile
			420					425					430		
Gly	Val	Lys	Thr	Val	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Glu
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Arg	Lys	Gly	Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly
	450					455					460				
Gly	Lys	Gly	Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	Gly
465					470					475					480
Leu	Glu	Ser	Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala
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Ser	Thr	Ser	Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	Thr
			500					505					510		
Leu	Ser	Phe	Ser	Val	Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	Gly
		515					520					525			
Gly	Gly	Leu	Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	Lys
		530				535					540				
Lys	Pro	Asn	Lys	Leu	Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	Pro
545					550					555					560
Ala	Glu	Ser	Ser	Ile	Ala	Thr	Trp	His	Gly	Asp	Asp	Phe	Lys	Asp	Lys
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Leu	Asn	Leu	Lys	Glu	Ser	Asp	Asp	Ser	Val	Asn	Thr	Glu	Asp	Arg	Ile
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Leu	Lys	Pro	Cys	Ser	Thr	Pro	Ser	Asp	Lys	Leu	Val	Ile	Asp	Lys	Leu
		595					600					605			
Val	Val	Asn	Phe	Gly	Asn	Val	Leu	Gln	Glu	Ile	Phe	Thr	Asp	Glu	Ala
	610					615					620				
Arg	Thr	Gly	Gln	Glu	Asn	Asn	Leu	Gly	Gly	Glu	Lys	Asn	Gly	Thr	Arg
625					630					635					640
Ile	Leu	Ser	Ser	Cys	Pro	Thr	Ser	Ile							
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate polynucleotide sequence of SEQ ID NO:46

<221> misc_feature
 <222> (1)...(1947)
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 acntggwsnc cnggnaarga racnwsntay acncartaya cngtnaarmg nacntaygcn 180
 ttyggngara arcaygayaa ytgyacnacn aaywsnwsna cnwsngaraa ymgngcnwsn 240
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 garaayggng ayggngtnat haarwsncay atgacntayt ggmngnytn ga raayathgcn 360
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 gcngayggnm gnmngccngt nmngnytnytn tggaraarg cnmgnggngc nccngtnytn 780
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 wsnatgathw sntayaayws nytnngnaar wsncngtng cnacnytnmg nathccngcn 960
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 gayaarytng tnathgayaa rytngtngtn aaytyggna aygtnytnca rgarathtty 1860
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 <213> Homo sapiens

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gaatgtccgc aaaacattag tttcactctt gtcgccaggt tggagtacaa tggcacgac      180
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gtgctgtggg aggtggagtt gcctttgatg caaatccttt gagccagcag aacatctgtg      480
gaacatcccc tgatac atg aag ctc tct ccc cag cct tca tgt gtt aac ctg      532
                Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu
                  1              5              10

ggg atg atg tgg acc tgg gca ctg tgg atg ctc cct tca ctc tgc aaa      580
Gly Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys
    15              20              25

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acc agt tat acc cag tac aca gtt aag aga act tac gct ttt gga gaa Thr Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu 65 70 75	724
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Pro	Glu	Ser	Asn	Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	
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cag	ctt	gaa	ctg	cat	ctg	gga	ggc	gag	agc	ttt	tgg	gtg	tct	atg	att	1444
Gln	Leu	Glu	Leu	His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	
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tct	tat	aat	tct	ctt	ggg	aag	tct	cca	gtg	gcc	acc	ctg	agg	att	cca	1492
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Val	Asn	Thr	Trp	Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	
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Thr	Thr	Leu	Ser	Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	
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Gln	Gln	Asp	Lys	Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	
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Gly	Gly	Lys	Gly	Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	
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Gly	Leu	Glu	Ser	Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	
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ggg gga ggc ctt ctt att ctc att atc ctg aca gtg gca tat ggt ctc 2164
 Gly Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu
 545 550 555

aaa aaa ccc aac aaa ttg act cat ctg tgt tgg ccc acc gtt ccc aac 2212
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 560 565 570

cct gct gaa agt agt ata gcc aca tgg cat gga gat gat ttc aag gat 2260
 Pro Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp
 575 580 585

aag cta aac ctg aag gag tct gat gac tct gtg aac aca gaa gac agg 2308
 Lys Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg
 590 595 600

atc tta aaa cca tgt tcc acc ccc agt gac aag ttg gtg att gac aag 2356
 Ile Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys
 605 610 615 620

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 640 645 650

aga att ctg tct tcc tgc cca act tca ata taagtgtgga ctaaaatgcg 2502
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 655 660

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<212> PRT

<213> Homo sapiens

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 35 40 45
 Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
 50 55 60
 Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
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 Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe

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Glu	Leu	Ala	Pro	Val 165	Ser	Ser	Asp	Leu	Lys 170	Tyr	Thr	Leu	Arg	Phe 175	Arg
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Cys	Gly	Leu	Glu	Leu 245	Trp	Arg	Val	Leu	Lys 250	Pro	Ala	Glu	Ala	Asp 255	Gly
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Ala	Gly	Gly 515	Thr	Asn	Gly	Thr	Ser 520	Ile	Asn	Phe	Lys	Thr 525	Leu	Ser	Phe
Ser	Val 530	Phe	Glu	Ile	Ile	Leu 535	Ile	Thr	Ser	Leu	Ile 540	Gly	Gly	Gly	Leu
Leu 545	Ile	Leu	Ile	Ile	Leu 550	Thr	Val	Ala	Tyr	Gly 555	Leu	Lys	Lys	Pro	Asn 560
Lys	Leu	Thr	His 565	Leu	Cys	Trp	Pro	Thr	Val 570	Pro	Asn	Pro	Ala	Glu	Ser
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<220>
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aarytnacnc	ayytntgytg	gccnacngtn	ccnaayccng	cngarwsnws	nathgcnaacn	1740
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acngargaym	gnathytnaa	rccntgywsn	acnccnwsng	ayaarytngt	nathgayaar	1860
ytngtngtna	ayttyggnaa	ygtnytnear	garathttya	cngaygargc	nmgnacnggn	1920
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	Met
	1
ctg agc agc cag aag gga tcc tgc agc cag gaa cca ggg gca gcc cac	287
Leu Ser Ser Gln Lys Gly Ser Cys Ser Gln Glu Pro Gly Ala Ala His	
	5 10 15
gtc cag cct ctg ggt gtg aac gct gga ata atg tgg acc ttg gca ctg	335
Val Gln Pro Leu Gly Val Asn Ala Gly Ile Met Trp Thr Leu Ala Leu	
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Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro Thr	
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aag cca gag aac att tcc tgc gtc ttt tac ttc gac aga aat ctg act	431
Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu Thr	
	50 55 60 65
tgc act tgg aga cca gag aag gaa acc aat gat acc agc tac att gtg	479
Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile Val	
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Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala Thr	
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Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp Ile	
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Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys Ser	
	115 120 125
gac atc aca tat tgg cat tta atc tcc ata gca aaa acc gaa cca cct	671
Asp Ile Thr Tyr Trp His Leu Ile Ser Ile Ala Lys Thr Glu Pro Pro	
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Ile Ile Leu Ser Val Asn Pro Ile Cys Asn Arg Met Phe Gln Ile Gln	
	150 155 160
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Trp Lys Pro Arg Glu Lys Thr Arg Gly Phe Pro Leu Val Cys Met Leu	
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Arg Phe Arg Thr Val Asn Ser Ser Arg Trp Thr Glu Val Asn Phe Glu	
	180 185 190

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Asn	Cys	Lys	Gln	Val	Cys	Asn	Leu	Thr	Gly	Leu	Gln	Ala	Phe	Thr	Glu	
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Tyr	Val	Leu	Ala	Leu	Arg	Phe	Arg	Phe	Asn	Asp	Ser	Arg	Tyr	Trp	Ser	
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Lys	Trp	Ser	Lys	Glu	Glu	Thr	Arg	Val	Thr	Met	Glu	Glu	Val	Pro	His	
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gtc	ctg	gac	ctg	tgg	aga	att	ctg	gaa	cca	gca	gac	atg	aac	gga	gac	1007
Val	Leu	Asp	Leu	Trp	Arg	Ile	Leu	Glu	Pro	Ala	Asp	Met	Asn	Gly	Asp	
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Arg	Lys	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	Leu	
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Glu	Lys	Thr	Phe	Gly	Tyr	His	Ile	Gln	Tyr	Phe	Ala	Glu	Asn	Ser	Thr	
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Gly	Lys	Ser	Gln	Glu	Thr	Ile	Leu	Arg	Ile	Pro	Asp	Val	His	Glu	Lys	
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Thr	Phe	Gln	Tyr	Ile	Lys	Ser	Met	Gln	Ala	Tyr	Ile	Ala	Glu	Pro	Leu	
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Leu	Val	Val	Asn	Trp	Gln	Ser	Ser	Ile	Pro	Ala	Val	Asp	Thr	Trp	Ile	
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Val	Glu	Trp	Leu	Pro	Glu	Ala	Ala	Met	Ser	Lys	Phe	Pro	Ala	Leu	Ser	
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cta	aaa	cct	ttc	aca	tgc	tat	aat	ata	tca	gtg	tat	cca	gtg	ttg	gga	1487
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His	Arg	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala	Lys	Glu	Gly	
		420					425					430				
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Thr 435	Pro	Leu	Lys	Gly	Pro	Glu 440	Thr	Arg	Val	Glu	Asn 445	Ile	Gly	Leu	Arg		
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ctc Leu	tcc Ser	aag Lys	act Thr 485	gtt Val	aac Asn	tct Ser	cat His	gcc Ala 490	ctg Leu	cag Gln	tgt Cys	gac Asp	ctg Leu 495	gag Glu	tct Ser	1727	
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cgg Arg	ttg Leu	act Thr	ccc Pro 565	ctg Leu	tgt Cys	tgt Cys	cct Pro	gat Asp 570	gtt Val	ccc Pro	aac Asn	cct Pro	gct Ala 575	gaa Glu	agt Ser	1967	
agt Ser	tta Leu	gcc Ala 580	aca Thr	tgg Trp	ctc Leu	gga Gly	gat Asp 585	ggg Gly	ttc Phe	aag Lys	aag Lys	tca Ser 590	aat Asn	atg Met	aag Lys	2015	
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ccc Pro 610	gtc Val	ccc Pro	gcg Ala	gat Asp	ctc Leu 615	att Ile	gac Asp	aag Lys	ctg Leu	gta Val 620	gtg Val	aac Asn	ttt Phe	gag Glu	aat Asn 625	2111	
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tgt Cys	cct Pro	ggc Gly 660	cat His	tgc Cys	tgaagctacc			ctcaggggtcc			aggacagctg			tcttggttggc		2262	
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Leu Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro
35      40      45
Thr Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu
50      55      60
Thr Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile
65      70      75      80
Val Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala
85      90      95
Thr Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp
100     105     110
Ile Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys
115     120     125
Ser Asp Ile Thr Tyr Trp His Leu Ile Ser Ile Ala Lys Thr Glu Pro
130     135     140
Pro Ile Ile Leu Ser Val Asn Pro Ile Cys Asn Arg Met Phe Gln Ile
145     150     155     160
Gln Trp Lys Pro Arg Glu Lys Thr Arg Gly Phe Pro Leu Val Cys Met
165     170     175
Leu Arg Phe Arg Thr Val Asn Ser Ser Arg Trp Thr Glu Val Asn Phe
180     185     190
Glu Asn Cys Lys Gln Val Cys Asn Leu Thr Gly Leu Gln Ala Phe Thr
195     200     205
Glu Tyr Val Leu Ala Leu Arg Phe Arg Phe Asn Asp Ser Arg Tyr Trp
210     215     220
Ser Lys Trp Ser Lys Glu Glu Thr Arg Val Thr Met Glu Glu Val Pro
225     230     235     240
His Val Leu Asp Leu Trp Arg Ile Leu Glu Pro Ala Asp Met Asn Gly
245     250     255
Asp Arg Lys Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
260     265     270
Leu Glu Lys Thr Phe Gly Tyr His Ile Gln Tyr Phe Ala Glu Asn Ser
275     280     285
Thr Asn Leu Thr Glu Ile Asn Asn Ile Thr Thr Gln Gln Tyr Glu Leu
290     295     300
Leu Leu Met Ser Gln Ala His Ser Val Ser Val Thr Ser Phe Asn Ser
305     310     315     320
Leu Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu
325     330     335
Lys Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro
340     345     350
Leu Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp
355     360     365
Ile Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu
370     375     380
Ser Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp

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385          390          395          400
Lys Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu
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Gly His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu
          420          425          430
Gly Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu
          435          440          445
Arg Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn
          450          455          460
Gly Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Gly Lys
465          470          475          480
Glu Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu
          485          490          495
Ser Leu Thr Arg Arg Thr Ser Tyr Thr Val Trp Val Met Ala Ser Thr
          500          505          510
Arg Ala Gly Gly Thr Asn Gly Val Arg Ile Asn Phe Lys Thr Leu Ser
          515          520          525
Ile Ser Val Phe Glu Ile Val Leu Leu Thr Ser Leu Val Gly Gly Gly
530          535          540
Leu Leu Leu Leu Ser Ile Lys Thr Val Thr Phe Gly Leu Arg Lys Pro
545          550          555          560
Asn Arg Leu Thr Pro Leu Cys Cys Pro Asp Val Pro Asn Pro Ala Glu
          565          570          575
Ser Ser Leu Ala Thr Trp Leu Gly Asp Gly Phe Lys Lys Ser Asn Met
          580          585          590
Lys Glu Thr Gly Asn Ser Gly Asn Thr Glu Asp Val Val Leu Lys Pro
          595          600          605
Cys Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu
610          615          620
Asn Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala
625          630          635          640
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21

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<220>
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36

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 <210> 68
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 <221> CDS
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 acc tgg gca ctg tgg atg ccc cct tca ctc tgc aaa ttc agc ctg gca 96
 Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala
 20 25 30
 gct ctg cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg 144
 Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
 35 40 45
 aaa aat tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc 192
 Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
 50 55 60
 cag tac aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat 240
 Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
 65 70 75 80
 tgt aca acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt 288
 Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
 85 90 95
 ttc ctt cca aga ata acg atc cca gat aat tat acc att gag gtg gaa 336
 Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu
 100 105 110

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aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro 595 600 605			1824

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gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc      1920
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
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tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc      1968
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
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aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg      2016
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
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gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc      2064
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
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Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
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gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc      2160
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ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac      2256
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
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Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
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Lys Pro Glu	Asn Ile Ser	Cys Val Phe	Tyr Phe Asp	Arg Asn Leu	Thr	
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Cys Thr Trp	Arg Pro Glu	Lys Glu Thr	Asn Asp Thr	Ser Tyr Ile	Val	
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Met Leu Ser Ser Gln Lys Gly Ser Cys Ser Gln Glu Pro Gly Ala Ala
1 5 10 15
His Val Gln Pro Leu Gly Val Asn Ala Gly Ile Met Trp Thr Leu Ala
20 25 30
Leu Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro
35 40 45
Thr Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu
50 55 60
Thr Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile
65 70 75 80
Val Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala
85 90 95
Thr Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp
100 105 110
Ile Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys
115 120 125
Ser Asp Ile Thr Tyr Trp His Leu Ile Ser Ile Ala Lys Thr Glu Pro
130 135 140
Pro Ile Ile Leu Ser Val Asn Pro Ile Cys Asn Arg Met Phe Gln Ile
145 150 155 160
Gln Trp Lys Pro Arg Glu Lys Thr Arg Gly Phe Pro Leu Val Cys Met
165 170 175
Leu Arg Phe Arg Thr Val Asn Ser Ser Arg Trp Thr Glu Val Asn Phe
180 185 190
Glu Asn Cys Lys Gln Val Cys Asn Leu Thr Gly Leu Gln Ala Phe Thr
195 200 205
Glu Tyr Val Leu Ala Leu Arg Phe Arg Phe Asn Asp Ser Arg Tyr Trp
210 215 220
Ser Lys Trp Ser Lys Glu Glu Thr Arg Val Thr Met Glu Glu Val Pro
225 230 235 240
His Val Leu Asp Leu Trp Arg Ile Leu Glu Pro Ala Asp Met Asn Gly
245 250 255
Asp Arg Lys Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
260 265 270
Leu Glu Lys Thr Phe Gly Tyr His Ile Gln Tyr Phe Ala Glu Asn Ser
275 280 285
Thr Asn Leu Thr Glu Ile Asn Ile Thr Thr Gln Gln Tyr Glu Leu
290 295 300
Leu Leu Met Ser Gln Ala His Ser Val Ser Val Thr Ser Phe Asn Ser
305 310 315 320
Leu Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu
325 330 335
Lys Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro
340 345 350
Leu Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp
355 360 365
Ile Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu
370 375 380
Ser Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp
385 390 395 400
Lys Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu
405 410 415
Gly His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu

			420					425					430		
Gly	Thr	Pro	Leu	Lys	Gly	Fro	Glu	Thr	Arg	Val	Glu	Asn	Ile	Gly	Leu
			435					440					445		
Arg	Thr	Ala	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Ala	Arg	Asn
			450					455					460		
Gly	Phe	Ile	Asn	Asn	Tyr	Thr	Val	Phe	Tyr	Gln	Ala	Glu	Gly	Gly	Lys
			465					470					475		
Glu	Leu	Ser	Lys	Thr	Val	Asn	Ser	His	Ala	Leu	Gln	Cys	Asp	Leu	Glu
			485					490					495		
Ser	Leu	Thr	Arg	Arg	Thr	Ser	Tyr	Thr	Val	Trp	Val	Met	Ala	Ser	Thr
			500					505					510		
Arg	Ala	Gly	Gly	Thr	Asn	Gly	Val	Arg	Ile	Asn	Phe	Lys	Thr	Leu	Ser
			515					520					525		
Ile	Ser	Glu	Tyr	Trp	Leu	Gln	Ala	Ser	Phe	Trp	Ser	Leu	Leu	Arg	Val
			530					535					540		
Gly	Asn	Val													
			545												